

A		
-51	<u>MEQRGQMAPAASGARKREBPGPREARGARPGLRVPTLVLVVAAVLLVS</u>	-2
-1	<u>AESALITQQLAPQORVAPQOKRSSPSEGLCPFGHISEDGRDCISCKYG</u>	49
50	<u>QDYSTEHNOLLEPLCRCTRCDSGEVELSPCTTTRNTVCQCEGTFREEDSP</u>	99
100	<u>EMCRKCRITGCFRGMVKVGDCTPWSDIETCVHESGIIIGVTVAAVVLIVAV</u>	149
150	<u>FVCKSLNKKVLFYLEGICSGGGGDFERVDRSSQRPGAEDNVLNKIVSTL</u>	199
200	<u>QPTQVPEQEMEVOEPAEPTGVNMLSPGESEHLLPEPAEAKRSQRRRLVFA</u>	249
250	<u>NEGDPTETLRQCYPDDFADLVPTDSNEFLMKRLGLMDNKKLVAKAEAGHR</u>	299
300	<u>DTLYTMLIKVNVKTRGDASVHTLLDALETLGERLAKQKLEHLLSSGKFM</u>	349
350	YLEGMSADSAMS* 360	

B		
-63	<u>MOGVKERYFLFLGNSGDRAFRFPDGRGRVVRPRFTQDGVGNHTMARIPKTLK</u>	-14
-13	<u>VVVIVAVLLPVLAYSATTARQEEVPQQTVAPOQQRHSFKGECPAGSHRS</u>	37
38	EHTGACNPFCTEGVDYTNASNNHPSCTFPCTVCKSDQKHKSSCTMTRDTVCQ	87
88	CKEGTFRNENSPFEMCRKCSRCPSGEVQVSNCTSWDDIQCVEEFGANATVE	137
138	TAAAEETMTTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPAPAAE	187
188	ETMTTSPGTPAPAAEETMTTSPGTPASSHYLSCTIVGLIVLIVLLIVFV*	236

DR5	273	SWEPLMRKGLMDNRK.VAKAAAGHEDTLYTMGIKVVKRG.RDSEVH	320
DR4	356	SWDQLMRQL DTKMKID.VVRAGTAGFGDALYAMLMKVVNKRG.RNASTH	403
DR3	346	RNKKEEVERTIGLSREASTLEAVEVEIGH.FBDQOXEMLRNRQQQP...AGLG	391
TNFR-1	330	RNKKEEVERTIGLSDEHIDRLLELQNGECLREAOYSMTATRRRTTPREATLE	379
FAS	228	QVGEHMDKONGVNEAKIDRKNDNVQDTAEQKVQLLRNWHQLHGKKEE.YD	276
CAR1	269	EWAREGHALDLOQENDLY.LAEQHDVSCPEFFOMENTHNLNQCG.SKAEVN	313

DR5	321	TGDDAGETTLGERLAKQITE	339
DR4	404	TGDDAGETTLGERLAKQITE	422
DR3	392	AVYAKHEDRMGGDGCVE LR	410
TNFR-1	380	LQGRVARDMDLGLCLEOTE	398
FAS	277	THEDKDKKANDCTLAETIQ	293
CAR1	314	TGLETTFPRIGLSGVADITA	333

FIGS. 1A-C

D

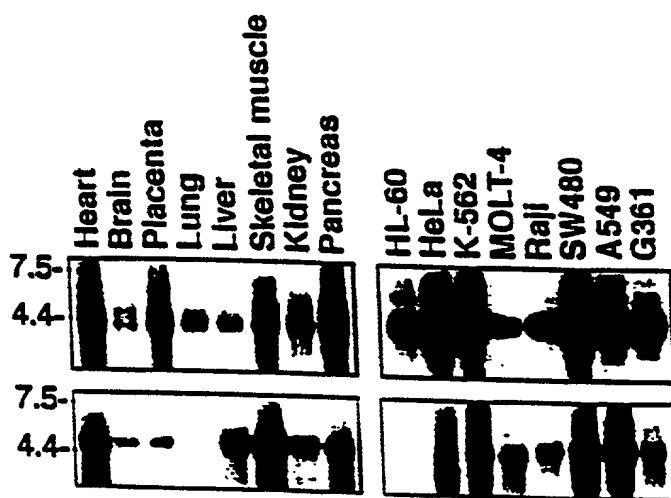


FIG. 1D

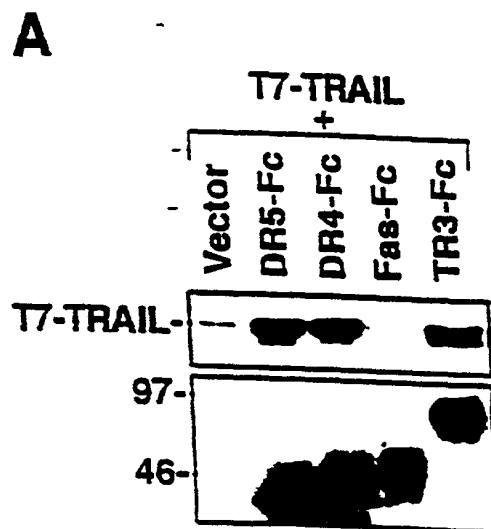


FIG. 2A

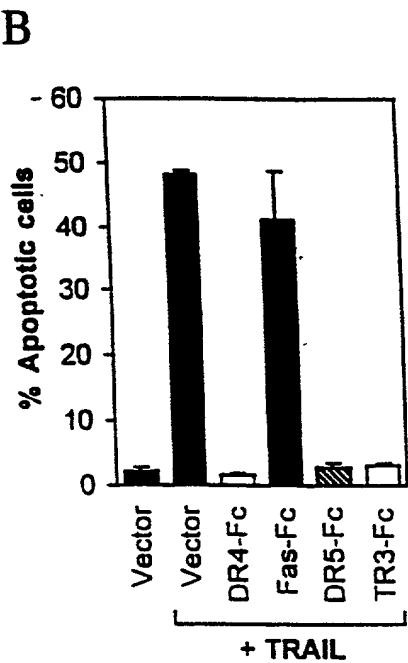
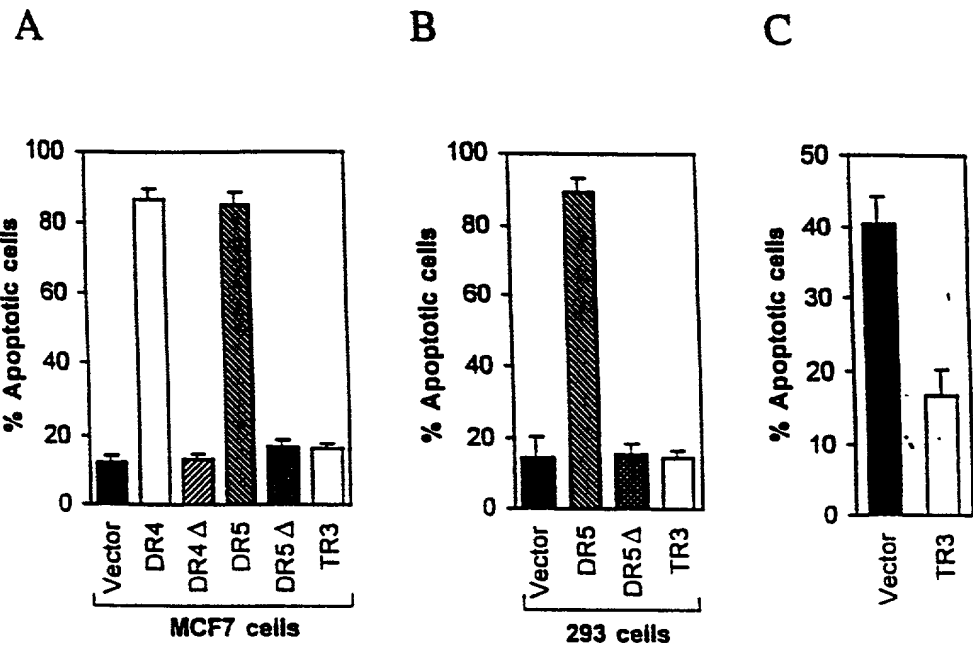
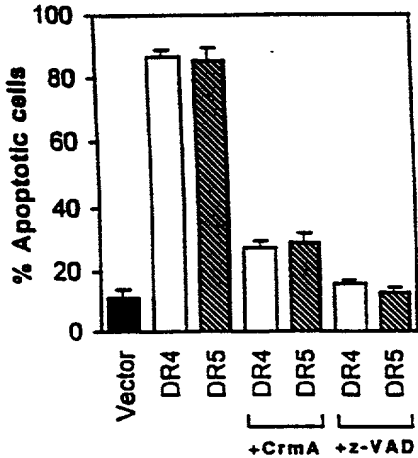


FIG. 2B

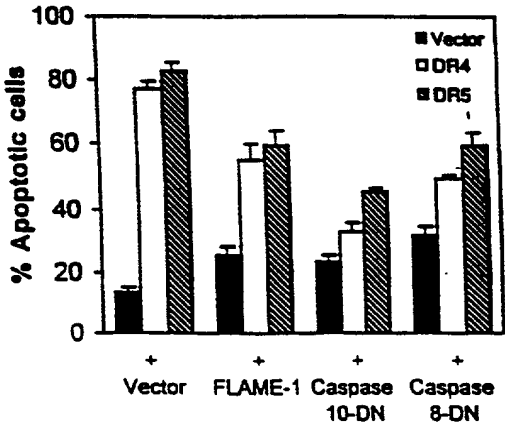


FIGS. 3A-C

D



E



FIGS. 3D-E

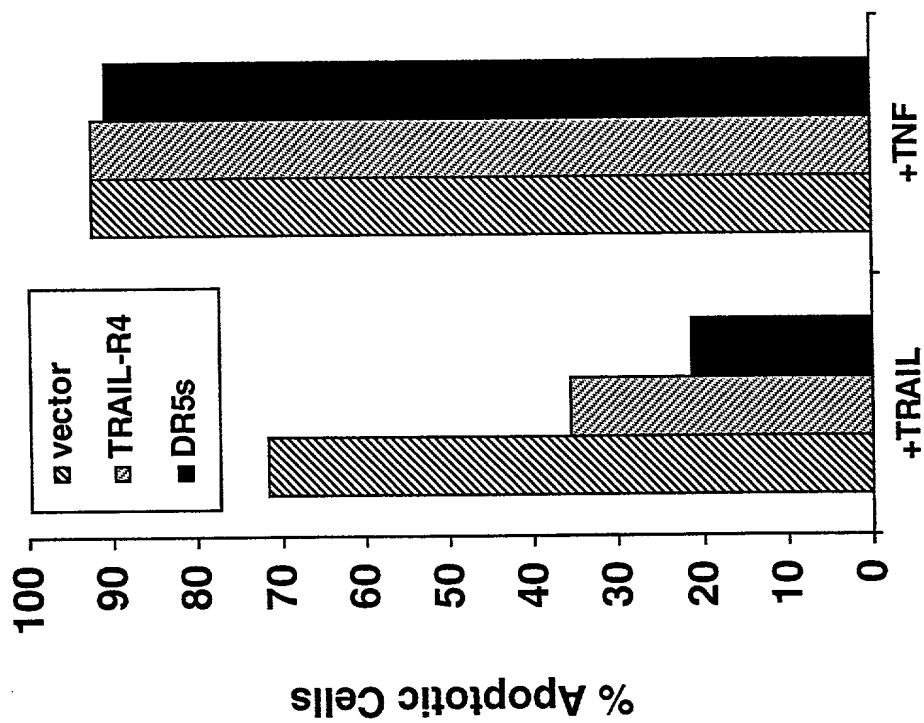
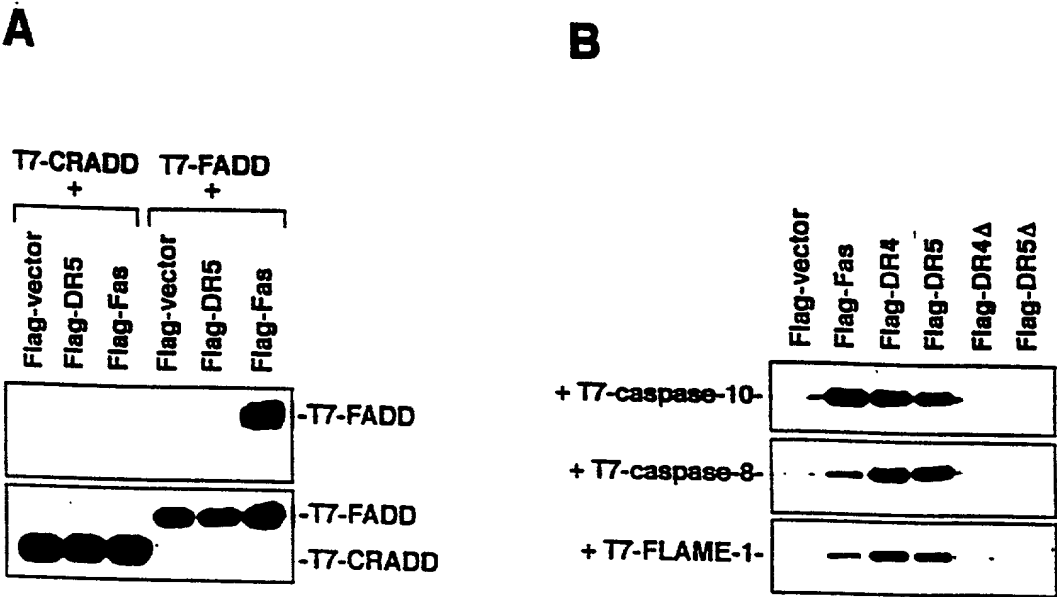


FIG. 3F



FIGS. 4A-B

1 ATGGAACAACGGGGACAGAACGCCCCGGCCGCTTCGGGGGGCCCGAAAGGCACGGCCCA 60
 1 M E Q R G Q N A P A A S G A R K R H G P 20

61 GGACCCAGGGAGGCGCGGGGAgCCAGGCCTGGGCTCCGGGTCCCCAAGACCCTTGTGCTC 120
 21 G P R E A R G A R P G L R V P K T L V L 40

121 GTTGTGCGCCGGTCTCTGCTGTTGGTCTCAGCTGAGTCTGCTCTGATCACCCAACAAGAC 180
 41 V V A A V L L L V S A E S A L I T Q Q D 60

181 CTAGCTCCCCAGCAGAGAGTGGCCCCACAACAAAAGAGGTCCAGCCCTCAGAGGGATTG 240
 61 L A P Q Q R V A P Q Q K R S S P S E G L 80

241 TGTCCACCTGGACACCATATCTCAGAAGACGGTAGAGATTGCATCTCTGCAAAATATGGA 300
 81 C P P G H H I S E D G R D C I S C K Y G 100

301 CAGGACTATAGCACTCACTGGAATGACCTCCTTTTCTGCTTGGCTGCACCAAGTGTGAT 360
 101 Q D Y S T H W N D L L F C L R C T R C D 120

361 TCAGGTGAAGTGGAGCTAAGTCCCTGCACCACGACCAGAAACACAGTGTGTGAGTGCAGAA 420
 121 S G E V E L S P C T T T R N T V C Q C E 140

421 GAAGGCACCTTCCGGGAAGAAGATTCTCCTGAGATGTGCCGGAAGTGCCGCACAGGGTGT 480
 141 E G T F R E E D S P E M C R K C R T G C 160

481 CCCAGAGGGATGGTCAAGGTCGGTGATTGTACACCCTGGAGTGACATCGAATGTGTCCAC 540
 161 P R G M V K V G D C T P W S D I E C V H 180

541 AAAGAATCAGGTACAAAGCACAGTGGGAAGCCCCAGCTGTGGAGGAGACGGTGACCTCC 600
 181 K E S G T K H S G E A P A V E E T V T S 200

601 AGCCCAGGGACTCCTGCCTCTCCCTGTTCTCTCAGGCATCATCATAGGAGTCAAGTT 660
 201 S P G T P A S P C S L S G I I I G V T V 220

661 GCAGCCGTAGTCTTGATTGTGGCTGTGTTGTTTGAAGTCTTTACTGTGGAAGAAAGTC 720
 221 A A V V L I V A V F V C K S L L W K K V 240

721 CTTCTTACCTGAAAGGCATCTGCTCAGGTGGTGGTGGGGACCCTGAGCGTGTGGACAGA 780
 241 L P Y L K G I C S G G G G D P E R V D R 260

781 AGCTCACAACGACCTGGGGCTGAGGACAATGTCCTCAATGAGATCGTGAGTATCTTGCAG 840
 261 S S Q R P G A E D N V L N E I V S I L Q 280

841 CCCACCCAGGTCCCTGAGCAGGAAATGGAAGTCCAGGAGCCAGCAGAGCCAACAGGTGTC 900
 281 P T Q V P E Q E M E V Q E P A E P T G V 300

901 AACAAAACCGGGGAgATGCCTCTGTCCACACCCTGCTGGATGCCTTGGAGACgCTGGGA 960
 301 N K T G R D A S V H T L L D A L E T L G 320

961 gAgAgACTTGCCAAGCAGAAGATTGAGGACCACTTGTGTGAGCTCTGGAAAGTTTCATGTAT 1020
 321 E R L A K Q K I E D H L L S S G K F M Y 340

1021 CTAGAAGGTAATGCAGACTCTGCCATGTCCTAA 1053
 341 L E G N A D S A M S * 351

FIG. 5

[illegible]

FIG. 6